

87163

From: Slobodyansky, Elizabeth
Sent: Friday, February 21, 2003 11:28 PM
To: STIC-Biotech/ChemLib
Subject: 09/590,375

RECEIVED

FEB 24 2003

Please align SEQ ID NO:1 in the above application with SEQ ID NO: 4 in US 6,197,565.

Thank you.

Elizabeth Slobodyansky, PhD

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B. licheniformis

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Searcher: _____
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Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Slobodansky
04/15/98 375
USC1975C5

> 0 <
01 10 IntellGenetics
> 0 <

GENALIGN Multiple Sequence Alignment Program
Release 5.4

Mon 24 Feb 103 10:49:49-PST

Solution Parameters:

Amino Alphabet - Identity
Output line length - 80
Compress - Off
Histogram - Off
Randomization - Off
AMINO-Res-length - 2
Deletion-weight - 5.00
Length-factor - 0
Matching-weight - 1.00
NUCLEIC-Res-length - 4
Spread-factor - 50

Clustered order of selected sequences:

4. US-09-193-468-4 (1-483)
9. US-09-590-375-1 (1-480)

Region Alignment: (listed in clustered order)

```
US-09-193- 1 anLNGT1MOYfEMyMNDGQHWRLQndsaYLaengITAWIIPRAYKGSQADVGAYDL
-590- 1 dGLNGTmmQYEmhlienDQHMnRLhndbaAalsdaGITAIWIPRAYKGSQADVGAYDL
consensus --LNGT-MQY-EW---NDGQHW-RL--D-A-L---GITA-WIPRAYKG-SQADVGAYDL

US-09-193- 62 YDLGEFHOKGTVRTKYGTKGqelqsaIKSLhsFDINVGQDVVlnHKgGADATEDVCAveYp
-590- 62 YDLGEFHOKGTVRTKYGTKGqelqsaIKSLhsFDINVGQDVVlnHKgGADATEDVCAveYp
consensus YDLGEF-OKGTVRTKYGTK--L--AI-SL-S-DINVGQDVV-NHK-GAD-TE-V-AV-V-P

US-09-193- 123 adRatVISGehliKAmThPhPGKgsCTSDfKwMyhNEdGLDDesrklnrIYkFgqkwd
-590- 123 tnRwqdiSGaYLiDAmTgTfdFagRnnaySDfKwTfHfngQVMDqgrYqenhi ffrAntm
consensus --R---ISG---I-AWT--F-F-GR---YSDfKW-W-HF-G-DWD-----N-I--F-----W-

US-09-193- 184 WeVnENGNNDYDLmyadIDydhPdvAaeIKrWGLyaneLqLdGfRLDAVKHikPsfLRDM
-590- 184 WtVdEENGNNDYDLlgsnidfshPevqdeIKGWSWfcdELdLdGyRLDAIKHlPfwYtsDW
consensus W-V--ENGNYDL-----ID--HP-V--E-K-WG-W---EL-LDG-RLDA-KHI-F----DW

US-09-193- 245 VnHvRekLgkEmfVaeYqndIGALenYlnkcnfnhsVFDVPLhyqfhaastGCGGYDMR
-590- 245 VtHqRneadqdlFvYgveYkdbvGALefYldemNwemsIFDVPLInfyfyrASQGSYDMR
consensus V-H-R-----F-V-EYW--D-GALE-YL---N--S-FDVPL-Y-F--AS-QGG-YDMR

US-09-193- 306 kLlNGctvyskHP1kavTFVNDHNDTOPGSLestvgTWFKPLAYAFILTRREGSpqVfyGDM
-590- 306 nLlRGS1YeaHPhmhaVTTFVNDHNDTOPGSLesWadwFKPLAYAFILTRREGSpVnVfyGdy
consensus --L-G--V--HP---VTFVNDHNDTOPG-SLES-V--WFKPLAYA-ILTRRE-GYP-VfyGD-
```

```
US-09-193- 367 YGckgdsqreIPAlKKhlePILKARKqYAYGaQHDYFDHDIvGWTREGSSvANSGLA1
US-09-590- 367 YG 1pndIsakkdmIdelldARqnYAYGtQHDYFDHvDvVGTREGSSfPNSGLA1
consensus YGckg-----I-A-K--I---L-AR--YAYG-QHDYFDH-D-VGWTREG-SS--NSGLA--
```

```
US-09-193- 428 ItdGPGakrMYVGRONAGetWdITGNrsepyVINseGGEFhVNGGSVsiYqr
US-09-590- 425 msnGPGsKwMYVGRONAGetWdITGNmngasVtlingdGGEFfLNGGSVSVYnq
consensus ---GPGG-K-MYVGRONAG-TW-D-TGN-----V-IN--GMGEF--NGGSVS-YV--
```

Alignment score = 286.00

Scoring matrix:

```

4 | 281
9 |
-----
```

> 0 <
0110 Intelligenetics
> 0 <

Results of the Initial Comparison of Sequences
Release 5.4

Results file us-09-193-068-4.res made by bshears on Mon 24 Feb 103 10:48:42-EST.

Query sequence being compared: US-09-193-068-4 (1-483)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the Initial Comparison of US-09-193-068-4 (1-483) with:
File: /home/bshears/slob*.pep

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
S -
SCORE 0 31 61 92 123 153 184 215 245 276
STDEV

PARAMETERS

Similarity matrix Unitary 1 K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 32
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 276 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 480
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Sig. Frame
Init. Opt.

1. US-09-590-375-1 Sequence 1, Application US 480 276 301 0.00 0
US-09-193-068-4 (1-483)
US-09-590-375-1 Sequence 1, Application US/09590375

Sequence 1, Application US/09590375
GENERAL INFORMATION:
APPLICANT: ENDO, Kaji et al.
TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
FILE REFERENCE: 2173-0120P
CURRENT APPLICATION NUMBER: US/09/590,375
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: JP P1999-163569
PRIOR FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 23
SEQ ID NO: 1
LENGTH: 480
TYPE: PRT
ORGANISM: Bacillus sp. KSM-K38

Initial Score = 276 Optimized Score = 301 Significance = 0.00
Residue Identity = 628 Matches = 302 Mismatches = 178
Gaps = 3 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
ANLGLTMOYFEMWYRNDGOWHRLDNDASVLAHGTAVIPRAVYKTSQADVYGYADYLDGERHOKT
DGLNGTMOYFEMWYRNDGOWHRLDNDASVLAHGTAVIPRAVYKTSQADVYGYADYLDGERHOKT
X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
VRRYGTGKGELOSATKSLHSRDIVYGVGVYINHKSGADATEDYVAVEVDADRNRVSGEHLIKAWTHFHP
VRRYGTGKGELOSATKSLHSRDIVYGVGVYINHKSGADATEDYVAVEVDADRNRVSGEHLIKAWTHFHP
VRRYGTGKGELOSATKSLHSRDIVYGVGVYINHKSGADATEDYVAVEVDADRNRVSGEHLIKAWTHFHP
X 80 90 100 110 120 130 140

150 160 170 180 190 200 210
GRGTYSDFKMHWYHFDGTDWDESRKLNRIYKFGKAMDEVSNNVYLYKADIDYHPVAAIKRMG
GRGTYSDFKMHWYHFDGTDWDESRKLNRIYKFGKAMDEVSNNVYLYKADIDYHPVAAIKRMG
GRGTYSDFKMHWYHFDGTDWDESRKLNRIYKFGKAMDEVSNNVYLYKADIDYHPVAAIKRMG
X 150 160 170 180 190 200 210

220 230 240 250 260 270 280
TWYANLQDLGFRIDAVKHKIKFSFLRDMVNHVREKTKGEMFTVAEYVQNDLGALENTLNKTNFNSHVFYPL
TWYANLQDLGFRIDAVKHKIKFSFLRDMVNHVREKTKGEMFTVAEYVQNDLGALENTLNKTNFNSHVFYPL
TWYANLQDLGFRIDAVKHKIKFSFLRDMVNHVREKTKGEMFTVAEYVQNDLGALENTLNKTNFNSHVFYPL
X 220 230 240 250 260 270 280

290 300 310 320 330 340 350 360
HYOFHASTOGGGYDMRKLLNGTVYVSKHPLAKSTYFVNDHNTGOGSLESTVQWFKPLAYATLITREGSTPQ
HYOFHASTOGGGYDMRKLLNGTVYVSKHPLAKSTYFVNDHNTGOGSLESTVQWFKPLAYATLITREGSTPQ
HYOFHASTOGGGYDMRKLLNGTVYVSKHPLAKSTYFVNDHNTGOGSLESTVQWFKPLAYATLITREGSTPQ
X 290 300 310 320 330 340 350 360

370 380 390 400 410 420 430
VFYGDYGYGIPND--NISAKKMDIDELLAROMYAVGTODHDYDHDVGVGTREGSSSRNSGLATIMSNCP
VFYGDYGYGIPND--NISAKKMDIDELLAROMYAVGTODHDYDHDVGVGTREGSSSRNSGLATIMSNCP
VFYGDYGYGIPND--NISAKKMDIDELLAROMYAVGTODHDYDHDVGVGTREGSSSRNSGLATIMSNCP
X 370 380 390 400 410 420 430

440 450 460 470 480 X
GSAKMYVGRONAGETWHDITGNRSEPVYINSRGESEPHVNGSVSYIYOR
GSAKMYVGRONAGETWHDITGNRSEPVYINSRGESEPHVNGSVSYIYOR
GSAKMYVGRONAGETWHDITGNRSEPVYINSRGESEPHVNGSVSYIYOR
X 440 450 460 470 480